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SEQUENCE LISTING
<110> Leung, Shawn Shuit-on
<120> REDUCING IMMUNOGENICITIES OF IMMUNOGEOBLEINS BY
FRAMEWORK-PATCHING
<130» 655
<140> US 89/892,613
<141> 2001-06-27
 <170> PatentIn version 3.3
<210- 1
<211- 309
<212- DNA
<213- Artificial Sequence
<Z28h</p>
<Z23h FR-patched heavy chain variable region sequence (Full DWA Sequence) formed by joining the N- and C- terminal (SEQ 3 and 6) halves at the Kpel site.</p>
 <Z20-
<Z21- V_region
<Z22- (1)..(369)
 gaagtgoogo tgotggagto tgggggaggo ttagtgoago otggagggto ootgaggoto
 toctgtgcag cototggatt otocttoagt atotatgaca tgtottgagt togcoagsca 128
cogggoogg ggctggogtg ggtcgcotoc attagtagtg gtggtggtac cacctactat 188
coagacacty typoggacy attraccate technological atgressgas eterctylus 248
 ctgramatga acagtetgag ggtggaggac acagcettat attactgtgc angacatagt 300
 ggctacggta gtagctacgg ggttttgttt gcttactggg gccaagggac tctggtcact 368
 <210- 2
<211- 123
<212- PKT
<213- Chinaera sp.
 <400> 2
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 18 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ile Tyr
20 25 38
Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Tyr Ite Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 88
 Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys
 Ala Ang His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
100 105 110
 Trp Gly Gln Gly Thr Lew Vol Thr Vol Ser Ser
<210- 3
<211- 111
<212- DNA
<213- Artificial Sequence
 «ZZ3» N-template is a synthetic sense strand oligonacteotide encoding
amino acide 14-50 of the VH region (SEQ ID No. 2). The template
is PCR amplified by two primers (SEQ ID No. 4 and 5)
 <22%
<Z21> Y_region
<Z22> (1)..(111)
 of the 3 congregate contrasper contrasper sections and the contrasper cont
 atgictiggg ticgcoggc accgggmang gggctggagt gggtcgcata c
```

```
<210- 4
<211- 57
<212- DNA
<213- Artificial Sequence
422b

322 5' Primer is a synthetic sense-strand oligonuctorise excelling

arms acid 1.15 of the Wingson (310, 10 No. 2). The 3' and of

the primer overlaps with the 3'end of the template by 18

nucleotides.
 <Z28>
<Z21> primer_bind
<Z22> (1)..($7)
 <4005 4
gaugigeage tgetgaggie tgggggggge ttagtgeage etggagggie eetgagg 57
<210- 5
<211- 48
<212- DNA
<213- Artificial Sequence
 <220.

<225 3' Primer is a synthetic anti-sense-strand oligonucleotide

encoding anno acid 43-50 of the NH region(SQ ID No. 2). The

primer overlaps with the template by 21 nucleotides.
 <22% priner_bind 
<22% (1)..(48)
 gtaggtggta coaccaccac tactaatgta tgcgacccac tecagooc
 <210: 6
<211: 132
<212: DNA
<213: Artificial Sequence
 <223b C-terminal is a synthetic sense-strand oligonacleotide encoding
amino acid 68:111 of the VM region (SIQ ID No 2) The template is
POR-amplified by two primers (SIQ ID No 7 and 8)
 <228>
<221> V_region
<222> (1)..(132)
 ^{\rm c480s} 6 traccatct compagacau tyccompans tractytacc tyconatymu caytetysgg - 60
 atanamaca cancettata ttactataca anacatanta actacantas tanctacana 128
 gttttgtttg ct
<210» 7
<211» 60
<212» DNA
<213» Artificial Sequence
 <222b. 5: Primer is a synthetic sense-strand oligonucleotide encoding amino acid 55:74 of the VH region (SEQ ID No Z). The 3' end of the primer overlaps with the 5'end of the template by 21 nucleotides.</p>
 <22% | c22% | primer_bind | c22% | (1)...(68)
 ggtggtacco cotactatec agacactgtg aagagcogst teaccatete cagagacast 68
<210- 8
<211> 57
<212- DNA
<213- Artificial Sequence</pre>
 <223b 3' Primer is a synthetic anti-sense-strand oligonacteotide
encoding amino acid 165-123 of the NH region (StO ID No 2). The
primer and the template overlaps by 21 nucleotides.
 <2285
<2215 primer_bind
<2225 (1)..(57)
 <000- 8
tanamages stancement recettance continues assumes extenses estance. 57
<210> 9
<211> 321
<212> DNA
<213> Artificial Sequence
```

```
<22% 
FR-patched light chain variable region sequence formed by joining the N- and C-terminal (SIQ 11 and 14) halves at the Kpel site.
gatatecaga tgaccoagte tecotectee etgtetgeet etgtgggaga cagagtoace
ottogttgca gggcaagtca ggacattagc auttatttaa actggtatca gcagaaacca 128
ggtaaggete egasacteet gatetactae actagtatat tacacteagg agteceatea 188
aggiteagig geograggic iggaacagaa titactetea eeaftagete eelgeageea — 240
gasgatting concinent ingressing aghanouse throughput attragegas 300
<210> 18
<211> 187
<212> PRT
<213> Chingery sp.
<400> 10
Asp Tie Gin Met The Gin Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 18 15
Asp Arg Vol The Tie Ser Cys Arg Alo Ser Gin Asp Tie Ser Asm Tyr
20 ZS 38
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Fle
35 49 45
Tyr Tyr Thr Ser Ile Leu His Ser Gly Vol Pro Ser Ang Phe Ser Gly
S0 SS 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 98 05
The Phe Gly Gly Gly The Lys Vol Glu Ile Lys
<210> 11
<211> 108
<212> DNA
<213> Artificial Sequence
<223> N-template is a synthetic sense strand oligenacteotide encoding
entro acid 11-46 of the VL region (SEQ ID No. 18). The template
is PCR amplified by two primers (SEQ ID No. 12 and 13)
<Z286
<Z21> Y_region
<Z22> (1)..(188)
ctgtctgcct ctgtgggaga cagagtcacc attagttgca gggcaagtca ggacattagc 68
auttattas actgatatca geognoseco agtanggete eganacte
<210> 12
<211> 51
<212> DNA
<213> Artificial Sequence
<228b</p>
<223b 5' Priner is a synthetic sense-strand oligonucleatide encoding onino acid 1-17 of the Wi region (StQ 10 No.16). The 3' end of the priner overlaps with the 5'end of the template by 21 months for.</p>
<Z20>
<Z21> primer_bind
<Z22> (1)..(51)
<4005 12
gatatecaga tgaccoagte tecatectee etgtetgeet etgtgggaga e
                                                                                         51
<210- 13
<211- 48
<212- DNA
<213- Artificial Sequence
```

<220×

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<223» 3' Primer is a synthetic anti-sense-strand oligonucleotide
encoding amino acid 40-53. The primer and the template overlaps
by 18 nucleotides.
<22% c221> priner_bind c222> (1)..(40)
statectoat greateaute aspertites sesections
<210» 14
<211» 120
<213 120
<212 DNA
<213 Artificial Sequence
<22%

4223b C-terminal is a synthetic sense-strand oligonucleotide encoding

amino acid 59-98 of the VM region (SEQ ID No.10) The template is

PCR amplified by tow priners (SEQ ID No.15 and 16)
<2205
<221> Y_region
<222> (1), (120)
<800> 14
contragget treatagnes teastctage econositie circurcet teactrocte 68
cagocagaag attitigocac tiactitigo caacagagia atacgotico giggacgito 128
<210- 15
<211- 49
<212- DNA
<213- Artificial Sequence
<2235 5' Primer is a synthetic sense-strand oligonucleotide encoding
amino acid 50-65 of the VII region (SIQ ID No. 10). The 3' end of
the primer overlaps with the 5'end of the template by 21
nucleotides
<221> priner_bind
<222> (1)..(49)
<480> 15
ctaccoming anotheract coggasters atmagging agingcogn
<210b 16

<211b 48

<212b DNA =

<213b Artificial Sequence
<223b 3' Primer is a synthetic anti-sense-strand oligenucleotide
encoding amino acid 92-107 of the VH region (SEQ (D No 18)). The
primer and the template overlaps by 21 nucleotides.
<2285
<2215 primer_bind
<2225 (1)..(48)
oles- 16
tttgatttcc accttggtgc ctccaccgaa cgtccacgga agogtatt
<2105 17
<2115 371
<2125 DNA
<2135 Artificial Sequence
 <2235 FR patched heavy chain variable region sequence (Full DNA Sequence) formed by joining the N- and C- terminal (SEQ 19 and 22) halves at the Kpel site.</p>
<221> Y_region
<222> (1)..(371)
coggregate taggagette eggagetgag glomatange etgaggette aglamagete (8)
tectacomas ettetageta cocotttoce ogitacomia tgeoctgagit oeggeogect 128
cctggaaggg gcctggaatg gattggagct atttatccag gaaatggtga tactagttac 188
antragaest trangagous agreeatity artgragues autoriting consector 248
atgasgates gasgtatgsa statgsggsa tatgaggtat stheatgtga segstagas 300
tocastasta actaratasa ctarittaan tartaasani asaanaron tattarasti. 368
toctotgato a
                                                                                                         271
<210> 18
<211> 123
```

```
<212> PRT
<213> Chingery sp.
Glm Val Glm Leu Val Ala Ser Gly Ala Glu Val Asn Lys Pro Gly Ala
1 5 18 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
28 25 38
Asm Met His Trp Vol Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 49 45
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
58 68
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 76 88
Met Glin Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 98 95
Ala Arg Ser His Tyr Gly Ser Asn Tyr Val Asp Tyr Phe Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Asp
115 128
<210b 19
<211> 114
<212> DNA =
<213> Artificial Sequence
<22%

<22% Nitemplate is a symthetic sense strand oligonucleotide encoding

omino acids 12-00 of the NH region (SSQ ID No. 18). The template

is PCR-captified by two primers (SSQ ID No. 20 and 21)
<Z21> Y_region
<Z22> (1)..(114)
<480<sub>5</sub> 19
autoagectg gagecteagt gaaggtetee tgemaggett etggetacae atttaccagt
tacastatgc actgagtacg gcagcctcct ggaaggagcc tggaatggat taga
                                                                                                           114
<210> 28
<211> 57
<213 5/
<212 DNA
<213 Artificial Sequence
420b
222b 5' Primer (s. a symbolic series strend oligonuctorized excising
erine acid 1:15 of the Wingsion (SIO, 10 to 15). The 3' end of
the prises overlaps with the 5'end of the template by 24
nucleotides.
<220>
<221> priner_bind
<222> (1)..(57)
coggigeous tggtggette eggggetgag glouatauge etggggeete agtgaug
<2105 21
<2115 55
<2125 DNA
<2130 Artificial Sequence
<220b

<22b J' Priner is a synthetic anti-sense strand oligenucleotide

encoding amno acid 45-00 of the NH region (SIQ ID No 18). The

priner and the template overlaps by 21 nucleotides.
<22% primer_bind 
<22> (1)..(55)
tgtasctagt atcaccattt octggatasa tagotocaat contocagg cooct
                                                                                                          SS
<210b 22
<211b 126
<212b DNA
<213b Artificial Seguence
<2235 C-terminal is a synthetic sense strand oligonacleotide encoding
amino acid 70-111 of the VM region (SEQ ID No 18) The template is
POR amplified by tow princes (SEQ ID No 23 and 24)
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<228>
<221> Y_region
<222> (1)..(126)
tigactgcag acasatccic cagcacagcc tacatgcagc tcagcagtci gacatcigag 68
gactotycgg totaltacty typosystop cactarygia glasciacyt sysciacitt 128
                                                                                                126
<210- 23
<211- 61
<212- DNA
<213- Artificial Sequence
<223b 5' Primer is a synthetic sense strand oliganucteotide encoding artino acid 57-76 of the VH region (SEQ ID No 18). The 3' end of the primer overlaps with the 5'end of the template by 21 nucleotides.</p>
<221> primer_bind
<222> (1)..(61)
<400» 23
 tgatactagt tacaatcaga aattoongag caaggccaca ttgactgcag acaaatcctc
<210> 24
<211> 50
<212> DNA
<213> Artificial Sequence
<222b 3' Primer is a synthetic anti-sense-strand oligonacteotide
encoding amino acid 105 123 of the VH region (SEQ ID No 18). The
primer and the template overlaps by 21 nucleotides.
<22% primer_bind 
<222> (1)..(59)
tgatcagogg agactgtasc agtggtgcct tggccccagt agtcasagta gtctacgta
<210> 25
<211> 321
<212> DNA
<213> Artificial Sequence
<22% - 
<22% - FR patched light chain variable region sequence (full DMM Sequence) formed by joining the H- and C-terminal (SEQ 27 and 30) halves at the BopEI site.</p>
<220s
<221> Y_region
<222> (1)..(321)
gatatteauc teacacagte tecateaugt etttetgeat etgtggggga cagagteaca
attactigca gggccagcic asgittaagi ticalgcaci ggtaccagca gaagccagga
tectorocca auccetggat transpersor technocing ettergaagt certagtege 188
ttcagtggca gtgggtctgg gaccgagttc actctcacaa tcagcagttt gcagcctgaa 248
getttogcce citatitcig ocaloogigg oglagiance ogcicacgit oggigciggg 300
accaagetga cogttetacg g
                                                                                                321
<210 26
<211 187
<212 PRT
<213 Chinaera sp.
Asp Ite 6tn Leu Thr 6tn Ser Pro Ser Ser Leu Ser Ala Ser Yal 6ty
1 5 18 15
Asp Arg Vol The The Cys Arg Alo Ser Ser Ser Leu Ser Pho Met
28 25 30
His Trp Tyr Glm Glm Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 49 45
Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
58 68
```

```
Gly Ser Gly Thr Glu Phe Thr Leu Thr Tle Ser Ser Leu Gln Pro Glu
Asp Phe Ata Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr 85 90 95
Pine Gly Ala Gly Thir Lys Leu Thir Val Leu Arg
100 105
<210> 27
<211> 129
<212> DNA
<213> Artificial Sequence
<22b.

422b. W-tomplate is a synthetic sense-strand oligonacleotide encoding

omino acide 9-51 of the VL region (SQ ID No. 26). The tomplate

is PCR-amplified by two primers (SQ ID No. 28 and 29)
<220-
<221- Y_region
<220- (1), (129)
transfertt etgentetgt gggggaraga gtencastta ettgraggge cagetrangt
ttaagtttoa tycactyyta ccayooyaay coayyatoot occocaaaco ctygatttat 128
geoneatee
                                                                                                                    129
<2105 28
<2115 45
<2125 DNA
<2135 Artificial Sequence
220.
222b 5: Primer is a synthetic sense strend oligonucteotide excelling
enno exid 115 of the Wiregion (SU) [D No 26). The 3' end of
the primer overlaps with the 5'end of the template by 21
nucleotides.
<221> priner_bind
<222> (1)..(45)
c4885 28
gatattomic tememogite tecotemagi etitetgeni etgig
                                                                                                                  45
<210+ 29
<211+ 48
<212+ DNA
<213- Artificial Sequence
223- 3' Primer is a synthetic anti-sense-strand oligonacteotide
encoding amino acid 45-57. The primer and the template overlaps
by 21 nucleotides.
<2285
<221> primer_bind
<222> (1)..(48)
ggactoogga agcoaggitg gatgiggcat aaatcoagag
<2105 38

<2115 120

<2125 DNA

<2135 Artificial Sequence
<22th.</p>
<22th.</p>
<22th.</p>
C terminal is a synthetic sense strand oligenacteotide encoding erino acid 61-180 of the Wrington (StQ ID No. 25) The template is PUX-amplified by ten primers (StQ ID No. 31 and 32).
<221> V_region
<222> (1)..(128)
ttcagtggco gtgggtctgg gaccgagttc actctcacas tcagcagttt gcagcctgaa 68
getticgcce citatiicig coatcegigg egiogienic cycloscyti cyglycigeg 128
<210- 31
<211> 43
<212- DNA
<213- Artificial Sequence
220. S Priper is a symbolic cense strand oligonuclostic encoding
arms exid 54 67 in the VI region (SQ ID No. 18). The 3' end of
the primer ownelps with the 5'end of the template by 21
nucleotides.
```

```
<220b
<221> priner_bind
<222> (1)..(43)
o400- 31
ggcttcogga gtccctogtc gcttcogtag cagtgagtct ggg
                                                                                         43
<210- 32
<211- 42
<212- DNA
<213> Artificial Sequence
<228b
31 Primer is a synthetic anti-sense-strand oligonuclootide
encoding amino acid 04-107 of the VN region (SEQ 10 No 20). The
primer and the template overlaps by 21 nucleotides.
<Z20>
<Z21> primer_bind
<Z22> (1)..(42)
cogtagascy gtcagcttgg tcccagcacc gascytgagc gg
<210s 33
<211s 123
<212s PRT
<213s Antibody
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
28 25 38
Asp Met Ser Trp Vol Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Vol
35 40 45
Als Tyr Ite Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Yal
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 78 88
Leu Glin Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 98 95
Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Lew Phe Ala Tyr
100 105 110
Trp Gly Glm Gly Thr Lew Vol Thr Vol Ser Ala
115 128
<210- 34
<211- 187
<212- PKT
<213- Antibody
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15
Asp Arg Vol The Ile Ser Cys Arg Alo Ser Gln Asp Ile Ser Asn Tyr
28 25 38
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Vol Lys Leu Leu Ele
Tyr Tyr Thr Ser ILe Leu His Ser Gly Val Pro Ser Ang Phe Ser Gly
Se 60
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
GS 76 88
Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 98 95
The Phe Gly Gly Gly The Lys Leu Glu Ile Lys
<210- 35
<211- 123
<212- PRT
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<213> Immunoglobulin
Glu Val Gin Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly 1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ele Tyr
28 39
Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Yal
35 48 45
Ald Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Yel
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 75 88
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 96 96
Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
115 120
<2105 36
<2115 29
<2125 PRT
<2136 [mnunoglobulin
Glu Val Gin Leu Val Glu Ser Gly Gly Gly Leu Val Pro Gly Gly Ser
Leu Arg Leu Ser Cys Ala Thr Thr 6ty Phe Ala Phe Ser
<210> 37
<211> 38
<212> PRT
<213> [mnunoglobulin
Glm Val Glm Lew Val Glw Ser Gly Gly Gly Val Val Glm Pro Gly Arg
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser
28 ZS 38
<210b 38
<211> 38
<212> PRT
<213> Immunoglobulin
Glu Val Gin Leu Leu Glu Ser Gly Gly Gly Leu Val Gin Pro Gly Gly
1 S 18 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser
20 25 30
<210- 30
<211- 14
<212- PRT
<213- Imunoglobulin
Trp Val Arg Gin Ala Pro Gly Lys Gly Leu Giu Trp Val Ala
1 5 18
<210> 48
<211> 32
<212> PRT
<213> Immunoglobulin
<400> 48
Ang Phe Thr Ile Ser Ang Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1 5 18 15
Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg
28 39
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<210b 41
<211> 11
<212b PRT
<213b [mmunoglobulin
<400s 41
Trp Gly Gln Gly Thr Lew Vol Thr Vol Ser Thr
<210 42
<211 187
<212 PRT
<213 Imunoglobulin
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly 1 \ 5 \ 10 \ 15
Asp Arg Vol The Tie Ser Cys Arg Alo Ser Gin Asp Tie Ser Asm Tyr
28 25 39
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Vol Lys Leu Leu Ele
35 40 45
Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Ang Phe Ser Gly S0 $55$
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr I'le Ser Asn Leu Glu Glu Gl<br/>65 70\, 70\, 75\, 80\,
Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 98 95
The Phe Gly Gly Gly The Lys Leu Glu Ile Lys
100 105
<210- 43
<211- 23
<212- PRT
<213- Immunoglobulin
<400> 43
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly 1 \phantom{-}5\phantom{0} 19 \phantom{-}15\phantom{0}
Asp Ang Vol Thr Ite Ser Cys
20
<210- 44
<211- 15
<212- PRT
<213- Immunglobulin
<210b 45
<211> 32
<212> PRT
<2130 Immunoglobulin
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 S 18 15
Leu Thr Ite Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys
20 5 30
<210> 46
<211> 10
<212> PRT
<213> Immunoglobulin
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 18
<210: 47
<211: 123
<212: PRT
<213: Immunoglobulin
<400> 47
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Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr 100 105 110 Trp Gly Glm Gly Thr Leu Vol Thr Vol Ser Ser Asp Ile Gin Met Thr Gin Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Vol Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr 28 25 39 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ele Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Ang Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp The Phe Gly Gly Gly The Lys Vol Glu Ile Lys Gln Val Gln Leu Arg Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala 1 5 19 15 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Fle Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe S8 SS 60 Lys Gly Lys Ala Thr Lea Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr 65 75 AB Met Glm Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Ang Ser His Tyr Gly Ser Asn Tyr Val Asp Tyr Phe Asp Tyr Trp 100 105 110 Gly Gln Gly The The Leu The Val Ser Ser Asp

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<210> 58
<211> 187
<212> PRT
<213> Immunoglobulin
Glm Ile Val Leu Ser Glm Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1 S 18 15
Glu Lys Vol Thr Met Thr Cys Ang Ala Ser Ser Ser Leu Ser Phe Met
28 25 39
His Trp Tyr Glm Glm Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45
Ala The See Asn Leu Ala See Gly Val Pro Ala Ang Phe See Gly See
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Tie Ser Arg Yol Glu Ala Glu
65 76 88
Asp Ata Ata Thr Tyr Phe Cys His 6th Trp Ser Ser Asn Pro Leu Thr
85 96 96
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
<210> 51
<211> 123
<212> PRT
<213> Immunoglobulin
Glm Val Gtm Leu Arg Glm Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 18 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
Asm Met His Trp Val Lys Glm Thr Pro Gly Glm Gly Leu Glu Trp Ele
35 40 45
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 78 88
Met Glin Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Yal Tyr Tyr Cys
Alu Arg Ser His Tyr Gly Ser Asn Tyr Val Asp Tyr Phe Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Asp
<2185 52
<2115 38
<2125 PRT
<2130 Immunoglobulin
Glm Val Glm Leu Val Ala Ser Gly Ala Glu Val Asm Lys Pro Gly Ala
1 S 18 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
<210- 53
<211- 14
<212- PRT
<213- Immunoglobulin
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210- 7

All 1 MP

All 1